What I claim is:

1. A method for typing HLA class I alleles, comprising the steps of:

-- amplifying HLA -A, -B, or -C alleles so as to provide a primary amplicon, wherein the primary amplicon comprises amplified exons 2 and 3 of the HLA -A, -B, or -C alleles in a locus specific manner;

-- producing at least two secondary HLA -A, -B, or -C locus specific amplicons corresponding to each of the exons 2 and 3 of the primary amplicon, wherein the at least two secondary amplicons are produced by amplifying the primary amplicon by means of using the primary amplicon as a template and nested polymerase chain reaction primers, thereby independently framing each of exon 2 and exon 3 with nested primers in the neighboring introns;

-- preparing the at least two secondary amplicons for sequencing, wherein the at least two secondary amplicons are provided with an anchoring moiety attached to a first terminus of each of the at least two secondary amplicons and a DNA sequencing primer site attached to a second terminus of each of the at least two secondary amplicons, wherein the DNA sequencing primer is a M13 universal primer;

-- attaching the anchoring moiety of each of the at least two secondary amplicons to solid supports; and

-- DNA sequencing each of the at least two secondary amplicons.

2. The method of claim 1, wherein the method further comprises the step of analyzing the DNA sequence of the at least two secondary amplicons so as to provide an HLA class type for the at least two secondary amplicons.

3. The method of claim 1, wherein in the step of preparing the at least two secondary amplicons, the anchoring moiety comprises a biotin molecule.

4. The method of claim 1, wherein the M13 universal primer is set forth in SEQ ID NO:1.

5. A method for determining tissue compatibility, comprising the steps of:

-- obtaining a sample of tissue, wherein the sample of tissue contains an amount of HLA -A, -B, or -C alleles;

-- amplifying the HLA -A, -B, or -C alleles so as to provide a primary amplicon, wherein the primary amplicon comprises amplified exons 2 and 3 of the HLA -A, -B, or -C alleles in a locus specific manner;

-- producing at least two secondary HLA -A, -B, or -C locus specific amplicons corresponding to each of the exons 2 and 3 of the primary amplicons, wherein the at least two secondary amplicons

are produced by amplifying the primary amplicon by means of using the primary amplicon as a template and nested polymerase chain reaction primers located in the introns bordering exons 2 and 3, thereby independently framing each of exon 2 and exon 3;

-- preparing the at least two secondary amplicons for sequencing, wherein the at least two secondary amplicons are provided with an anchoring moiety attached to a first terminus of each of the at least two secondary amplicons and a DNA sequencing primer site attached to a second terminus of each of the at least two secondary amplicons, wherein the DNA sequencing primer is a M13 universal primer;

-- attaching the anchoring moiety of each of the at least two secondary amplicons to solid supports;

-- DNA sequencing each of the at least two secondary amplicons; and

-- comparing the DNA sequence of the at least two secondary amplicons with at least one predetermined tissue sample.

6. The method of claim 5, wherein the M13 universal primer is set forth in SEQ ID NO:1.